

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Lau, Lester F.
- (ii) TITLE OF INVENTION: Extracellular Matrix Signalling Molecules
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
  - (B) STREET: 6300 Sears Tower, 233 South Wacker Drive
  - (C) CITY: Chicago
  - (D) STATE: Illinois
  - (E) COUNTRY: United States of America
  - (F) ZIP: 60606-6402
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Clough, David W.
  - (B) REGISTRATION NUMBER: 36,107
  - (C) REFERENCE/DOCKET NUMBER: 28758/33766
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 312/474-6300
  - (B) TELEFAX: 312/474-0448
  - (C) TELEX: 25-3856

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1480 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 180..1316
- (ix) FEATURE:
  - (A) NAME/KEY: misc feature
  - (D) OTHER INFORMATION: "Mouse cyr61 cDNA coding sequence"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
 

CGAGAGCGCC CCAGAGAAGC GCCTGCAATC TCTGCGCCTC CTCCGCCAGC ACCTCGAGAG	60
AAGGACACCC GCCGCCTCGG CCCTCGCCTC ACCGCACTEC GGGCGCATTT GATCCCGCTG	120

CTCGCCGGCT TGTGGTTCT GTGTCGCCGC GCTCGCCCCG GTTCCTCCTG CGCGCCACA	179
ATG AGC TCC AGC ACC TTC AGG ACG CTC GCT GTC GCC GTC ACC CTT CTC Met Ser Ser Ser Thr Phe Arg Thr Leu Ala Val Ala Val Thr Leu Leu	227
1 5 10 15	
CAC TTG ACC AGA CTG GCG CTC TCC ACC TGC CCC GCC GCC TGC CAC TGC His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys	275
20 25 30	
CCT CTG GAG GCA CCC AAG TGC GCC CCG GGA GTC GGG TTG GTC CGG GAC Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp	323
35 40 45	
GGC TGC GGC TGC TGT AAG GTC TGC GCT AAA CAA CTC AAC GAG GAC TGC Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys	371
50 55 60	
AGC AAA ACT CAG CCC TGC GAC CAC ACC AAG GGG TTG GAA TGC AAT TTC Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe	419
65 70 75 80	
GGC GCC AGC TCC ACC GCT CTG AAA GGG ATC TGC AGA GCT CAG TCA GAA Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu	467
85 90 95	
GGC AGA CCC TGT GAA TAT AAC TCC AGA ATC TAC CAA AAC GGG GAA AGC Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser	515
100 105 110	
TTC CAG CCC AAC TGT AAA CAC CAG TGC ACA TGT ATT GAT GGC GCC GTG Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val	563
115 120 125	
GGC TGC ATT CCT CTG TGT CCC CAA GAA CTG TCT CTC CCC AAT CTG GGC Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly	611
130 135 140	
TGT CCC AAC CCC CGG CTG GTG AAA GTC AGC GGG CAG TGC TGT GAA GAG Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly Gln Cys Cys Glu Glu	659
145 150 155 160	
TGG GTT TGT GAT GAA GAC AGC ATT AAG GAC TCC CTG GAC GAC CAG GAT Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Ser Leu Asp Asp Gln Asp	707
165 170 175	
GAC CTC CTC GGA CTC GAT GCC TCG GAG GTG GAG TTA ACG AGA AAC AAT Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn	755
180 185 190	
GAG TTA ATC GCA ATT GGA AAA GGC AGC TCA CTG AAG AGG CTT CCT GTC Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val	803
195 200 205	
TTT GGC ACC GAA CCG CGA GTT CTT TTC AAC CCT CTG CAC GCC CAT GGC Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro Leu His Ala His Gly	851
210 215 220	
CAG AAA TGC ATC GTT CAG ACC ACG TCT TGG TCC CAG TGC TCC AAG AGC Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser	899
225 230 235 240	
TGC GGA ACT GGC ATC TCC ACA CGA GTT ACC AAT GAC AAC CCA GAG TGC	947

Cys Gly Thr Gly	Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys	
	245 250 255	
CGC CTG GTG AAA GAG ACC CGG ATC TGT GAA GTG CGT CCT TGT GGA CAA		995
Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln	260 265 270	
CCA GTG TAC AGC AGC CTA AAA AAG GGC AAG AAA TGC AGC AAG ACC AAG		1043
Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys	275 280 285	
AAA TCC CCA GAA CCA GTC AGA TTT ACT TAT GCA GGA TGC TCC AGT GTC		1091
Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val	290 295 300	
AAG AAA TAC CGG CCC AAA TAC TGC GGC TCC TGC GTA GAT GGC CGG TGC		1139
Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys	305 310 315 320	
TGC ACA CCT CTG CAG ACC AGA ACT GTG AAG ATG CGG TTC CGA TGC GAA		1187
Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu	325 330 335	
GAT GGA GAG ATG TTT TCC AAG AAT GTC ATG ATG ATC CAG TCC TGC AAA		1235
Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys	340 345 350	
TGT AAC TAC AAC TGC CCG CAT CCC AAC GAG GCA TCG TTC CGA CTG TAC		1283
Cys Asn Tyr Asn Cys Pro His Pro Asn Glu Ala Ser Phe Arg Leu Tyr	355 360 365	
AGC CTA TTC AAT GAC ATC CAC AAG TTC AGG GAC TAAGTGCCTC CAGGGTTCCT		1336
Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp	370 375	
AGTGTGGGCT GGACAGAGGA GAAGCGCAAG CATCATGGAG ACGTGGGTGG GCGGAGGATG		1396
AATGGTGCCT TGCTCATTCT TGAGTAGCAT TAGGGTATTT CAAAACTGCC AAGGGGCTGA		1456
TGTGGACGGA CAGCAGCGCA GCCG		1480

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (D) OTHER INFORMATION: "Mouse Cyr61 amino acid sequence"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Ser	Ser	Thr	Phe	Arg	Thr	Leu	Ala	Val	Ala	Val	Thr	Leu	Leu
1				5					10					15	
His	Leu	Thr	Arg	Leu	Ala	Leu	Ser	Thr	Cys	Pro	Ala	Ala	Cys	His	Cys
		20					25						30		
Pro	Leu	Glu	Ala	Pro	Lys	Cys	Ala	Pro	Gly	Val	Gly	Leu	Val	Arg	Asp

- 4 -

370

375

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 124..1266

## (ix) FEATURE:

- (A) NAME/KEY: misc feature
- (D) OTHER INFORMATION: "Human cyr61 cDNA coding sequence"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

GGGCGGGCCC ACCGCGACAC CGCGCCGCCA CCCCACCCCC GCTGCGCACG GCCTGTCCGC      60
TGCACACCAG CTTGTTGGCG TCTTCGTCGC CGCGCTCGCC CCGGGCTACT CCTGCGCGCC      120
ACA ATG AGC TCC CGC ATC GCC AGG GCG CTC GCC TTA GTC GTC ACC CTT      168
  Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu
    1             5             10             15
CTC CAC TTG ACC AGG CTG GCG CTC TCC ACC TGC CCC GCT GCC TGC CAC      216
Leu His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His
                20             25             30
TGC CCC CTG GAG GCG CCC AAG TGC GCG CCG GGA GTC GGG CTG GTC CGG      264
Cys Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg
                35             40             45
GAC GGC TGC GGC TGC TGT AAG GTC TGC GCC AAG CAG CTC AAC GAG GAG      312
Asp Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp
    50             55             60
TGC AGC AAA ACG CAG CCC TGC GAC CAC ACC AAG GGG CTG GAA TGC AAC      360
Cys Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn
    65             70             75
TTC GGC GCC AGC TCC ACC GCT CTG AAG GGG ATC TGC AGA GCT CAG TCA      408
Phe Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser
    80             85             90             95
GAG GGC AGA CCC TGT GAA TAT AAC TCC AGA ATC TAC CAA AAC GGG GAA      456
Glu Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu
                100             105             110
AGT TTC CAG CCC AAC TGT CAA CAT CAG TGC ACA TGT ATT GAT GGC GCC      504
Ser Phe Gln Pro Asn Cys Gln His Gln Cys Thr Cys Ile Asp Gly Ala
                115             120             125
GTG GGC TGC ATT CCT CTG TGT CCC CAA GAA CTA TCT CTC CCC AAC TTG      552
Val Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu
                130             135             140
GGC TGT CCC AAC CCT CGG CTG GTC AAA GTT ACC GGG CAG TGC TGC GAG      600

```

Gly 145	Cys	Pro	Asn	Pro	Arg	Leu 150	Val	Lys	Val	Thr	Gly 155	Gln	Cys	Cys	Glu	
GAG 160	TGG Trp	GTC Val	TGT Cys	GAC Asp	GAG Glu	GAT Asp	AGT Ser	ATC Ile	AAG Lys	GAC Asp	CCC Pro	ATG Met	GAG Glu	GAC Asp	CAG Gln	648
GAC Asp	GGC Gly	CTC Leu	CTT Leu	GGC Gly	AAG Lys	GAG Glu	CTG Leu	GGA Gly	TTC Phe	GAT Asp	GCC Ala	TCC Ser	GAG Glu	GTG Val	GAG Glu	696
TTG Leu	ACG Thr	AGA Arg	AAC Asn	AAT Asn	GAA Glu	TTG Leu	ATT Ile	GCA Ala	GTT Val	GGA Gly	AAA Lys	GGC Gly	AGA Arg	TCA Ser	CTG Leu	744
AAG Lys	CGG Arg	CTC Leu	CCT Pro	GTT Val	TTT Phe	GGA Gly	ATG Met	GAG Glu	CCT Pro	CGC Arg	ATC Ile	CTA Leu	TAC Tyr	AAC Asn	CCT Pro	792
TTA Leu	CAA Gln	GGC Gly	CAG Gln	AAA Lys	TGT Cys	ATT Ile	GTT Val	CAA Gln	ACA Thr	ACT Thr	TCA Ser	TGG Trp	TCC Ser	CAG Gln	TGC Cys	840
TCA Ser	AAG Lys	ACC Thr	TGT Cys	GGA Gly	ACT Thr	GGT Gly	ATC Ile	TCC Ser	ACA Thr	CGA Arg	GTT Val	ACC Thr	AAT Asn	GAC Asp	AAC Asn	888
CCT Pro	GAG Glu	TGC Cys	CGC Arg	CTT Leu	GTG Val	AAA Lys	GAA Glu	ACC Thr	CGG Arg	ATT Ile	TGT Cys	GAG Glu	GTG Val	CGG Arg	CCT Pro	936
TGT Cys	GGA Gly	CAG Gln	CCA Pro	GTG Val	TAC Tyr	AGC Ser	AGC Ser	CTG Leu	AAA Lys	AAG Lys	GGC Gly	AAG Lys	AAA Lys	TGC Cys	AGC Ser	984
AAG Lys	ACC Thr	AAG Lys	AAA Lys	TCC Ser	CCC Pro	GAA Glu	CCA Pro	GTC Val	AGG Arg	TTT Phe	ACT Thr	TAC Tyr	GCT Ala	GGA Gly	TGT Cys	1032
TTG Leu	AGT Ser	GTG Val	AAG Lys	AAA Lys	TAC Tyr	CGG Arg	CCC Pro	AAG Lys	TAC Tyr	TGC Cys	GGT Gly	TCC Ser	TGC Cys	GTG Val	GAC Asp	1080
GGC Gly	CGA Arg	TGC Cys	TGC Cys	ACG Thr	CCC Pro	CAG Gln	CTG Leu	ACC Thr	AGG Arg	ACT Thr	GTG Val	AAG Lys	ATG Met	CGG Arg	TTC Phe	1128
CGC Arg	TGC Cys	GAA Glu	GAT Asp	GGG Gly	GAG Glu	ACA Thr	TTT Phe	TCC Ser	AAG Lys	AAC Asn	GTC Val	ATG Met	ATG Met	ATC Ile	CAG Gln	1176
TCC Ser	TGC Cys	AAA Lys	TGC Cys	AAC Asn	TAC Tyr	AAC Asn	TGC Cys	CCG Pro	CAT His	GCC Ala	AAT Asn	GAA Glu	GCA Ala	GCG Ala	TTT Phe	1224
CCC Pro	TTC Phe	TAC Tyr	AGG Arg	CTG Leu	TTC Phe	AAT Asn	GAC Asp	ATT Ile	CAC His	AAA Lys	TTT Phe	AGG Arg	GAC Asp			1266
TAAATGCTAC	CTGGGTTTCC	AGGGCACACC	TAGACAAACA	AGGGAGAAGA	GTGTCAGAAT											1326
CAGAATCATG	GAGAAAATGG	GCGGGGGTGG	TGTGGGTGAT	GGGACTCATT	GTAGAAAGGA											1386

AGCCTTCTCA TTCTTGAGGA GCATTAAGGT AT

1418

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(D) OTHER INFORMATION: "Human Cyr61 amino acid sequence"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu Leu
 1           5           10           15
His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys
          20           25           30
Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp
          35           40           45
Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys
          50           55           60
Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe
          65           70           75           80
Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu
          85           90           95
Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser
          100          105          110
Phe Gln Pro Asn Cys Gln His Gln Cys Thr Cys Ile Asp Gly Ala Val
          115          120          125
Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly
          130          135          140
Cys Pro Asn Pro Arg Leu Val Lys Val Thr Gly Gln Cys Cys Glu Glu
          145          150          155          160
Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Pro Met Glu Asp Gln Asp
          165          170          175
Gly Leu Leu Gly Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu Leu
          180          185          190
Thr Arg Asn Asn Glu Leu Ile Ala Val Gly Lys Gly Arg Ser Leu Lys
          195          200          205
Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro Leu
          210          215          220
Gln Gly Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser
          225          230          235          240
Lys Thr Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro

```

(2) INFORMATION FOR SEQ ID NO:5:

(A) LENGTH: 2267 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: misc feature

(D) OTHER INFORMATION: "Fisp12 cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCCGCC	GACAACCCCA	GACGCCACCG	CCTGGAGCGT	CCAGACACCA	ACCTCCGCCC	60
CTGTCCGAAT	CCAGGCTCCA	GCCGCGCCTC	TCGTGCGCTC	TGCACCCTGC	TGTGCATCCT	120
CCTACCGCGT	CCCGATCATG	CTCGCCTCCG	TCGCAGGTCC	CATCAGCCTC	GCCTTGGTGC	180
TCCTCGCCCT	CTGCACCCGG	CCTGCTACGG	GCCAGGACTG	CAGCGCGCAA	TGTCAGTGC	240
CAGCCGAAGC	AGCGCCGCAC	TGCECCGCCG	GCGTGAGCCT	GGTGCTGGAC	GGCTGCGGCT	300
GCTGCCGCGT	CTGCGCCAAG	CAGCTGGGAG	AACTGTGTAC	GGAGCGTGAC	CCCTGCGACC	360
CACACAAGGG	CCTCTTCTGC	GATTTCCGGCT	CCCCCGCCAA	CCGCAAGATT	GGAGTGTGCA	420
CTGCCAAAGA	TGGTGCACCC	TGTGTCTTCG	GTGGGTGCGT	GTACCGCAGC	GGTGAGTCCT	480
TCCAAAGCAG	CTGCAAATAC	CAATGCACTT	GCCTGGATGG	GGCCGTGGGC	TGCGTGCCCC	540
TATGCAGCAT	GGACGTGCGC	CTGCCCAGCC	CTGACTGCCC	CTTCCCGAGA	AGGGTCAAGC	600
TGCCTGGGAA	ATGCTGCAAG	GAGTGGGTGT	GTGACGAGCC	CAAGGACCGC	ACAGCAGTTG	660



GCCCTGCCCT	AGCTGCCTAC	CGACTGGAAG	ACACATTTGG	CCCAGACCCA	ACTATGATGC	720
GAGCCAACTG	CCTGGTCCAG	ACCACAGAGT	GGAGCGCCTG	TTCTAAGACC	TGTGGAATGG	780
GCATCTCCAC	CCGAGTTACC	AATGACAATA	CCTTCTGCAG	ACTGGAGAAG	CAGAGCCGCC	840
TCTGCATGGT	CAGGCCCTGC	GAAGCTGACC	TGGAGGAAAA	CATTAAGAAG	GGCAAAAAGT	900
GCATCCGGAC	ACCTAAAATC	GCCAAGCCTG	TCAAGTTTGA	GCTTTCTGGC	TGCACCAGTG	960
TGAAGACATA	CAGGGCTAAG	TTCTGCGGGG	TGTGCACAGA	CGGCCGCTGC	TGCACACCGC	1020
ACAGAACCAC	CACTCTGCCA	GTGGAGTTCA	AATGCCCCGA	TGGCGAGATC	ATGAAAAAGA	1080
ATATGATGTT	CATCAAGACC	TGTGCCTGCC	ATTACAACCTG	TCCTGGGGAC	AATGACATCT	1140
TTGAGTCCCT	GTAATACAGG	AAGATGTACG	GAGACATGGC	GTAAAGCCAG	GAAGTAAGGG	1200
ACACGAACTC	ATTAGACTAT	AACCTGAACT	GAGTTGCATC	TCATTTTCTT	CTGTAAAAAC	1260
AATTACAGTA	GCACATTAAT	TTAAATCTGT	GTTTTTAACT	ACCGTGGGAG	GAACATATCCC	1320
ACCAAAGTGA	GAACGTTATG	TCATGGCCAT	ACAAGTAGTC	TGTCAACCTC	AGACACTGGT	1380
TTGAGACAG	TTTACACTTG	ACAGTTGTTC	ATTAGCGCAC	AGTGCCAGAA	CGCACACTGA	1440
GGTGAGTCTC	CTGGAACAGT	GGAGATGCCA	GGAGAAAGAA	AGACAGGTAC	TAGCTGAGGT	1500
TATTTTAAAA	GCAGCAGTGT	GCCTACTTTT	TGGAGTGTA	CCGGGGAGGG	AAATTATAGC	1560
ATGCTTGCG	ACAGACCTGC	TCTAGCGAGA	GCTGAGCATG	TGTCCTCCAC	TAGATGAGGC	1620
TGAGTCCAGC	TGTTCTTTAA	GAACAGCAGT	TTCAGCCTCT	GACCATTCTG	ATTCCAGTGA	1680
CACTTGTCAG	GAGTCAGAGC	CTTGTCTGTT	AGACTGGACA	GCTTGTGGCA	AGTAAGTTTG	1740
CCTGTAACAA	GCCAGATTTT	TATTGATATT	GTAAATATTG	TGGATATATA	TATATATATA	1800
TATATTTGTA	CAGTTATCTA	AGTTAATTTA	AAGTCATTTG	TTTTTGTTTT	AAGTGCTTTT	1860
GGGATTTTAA	ACTGATAGCC	TCAAACCTCA	AACACCATAG	GTAGGACACG	AAGCTTATCT	1920
GTGATTCAAA	ACAAAGGAGA	TACTGCAGTG	GGAATTGTGA	CCTGAGTGAC	TCTCTGTCAG	1980
AACAAACAAA	TGCTGTGCAG	GTGATAAAGC	TATGTATTGG	AAGTCAGATT	TCTAGTAGGA	2040
AATGTGGTCA	AATCCCTGTT	GGTGAACAAA	TGGCCTTTAT	TAAGAAATGG	CTGGCTCAGG	2100
GTAAGGTCCG	ATTCCTACCA	GGAAGTGCTT	GCTGCTTCTT	TGATTATGAC	TGGTTTGGGG	2160
TGGGGGGCAG	TTTATTTGTT	GAGAGTGTGA	CCAAAAGTTA	CATGTTTGCA	CCTTTCTAGT	2220
TGAAAATAAA	GTATATATAT	ATTTTTTTATA	TGAAAAAAA	GGAATTC		2267

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (ix) FEATURE:

(A) NAME/KEY: misc feature

(D) OTHER INFORMATION: "Fispl2 amino acid sequence"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Met Leu Ala Ser Val Ala Gly Pro Ile Ser Leu Ala Leu Val Leu Leu
 1           5           10           15
Ala Leu Cys Thr Arg Pro Ala Thr Gly Gln Asp Cys Ser Ala Gln Cys
 20           25           30
Gln Cys Ala Ala Glu Ala Ala Pro His Cys Pro Ala Gly Val Ser Leu
 35           40           45
Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu Gly
 50           55           60
Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu Phe
 65           70           75           80
Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr Ala
 85           90           95
Lys Asp Gly Ala Pro Cys Val Phe Gly Gly Ser Val Tyr Arg Ser Gly
100           105           110
Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp Gly
115           120           125
Ala Val Gly Cys Val Pro Leu Cys Ser Met Asp Val Arg Leu Pro Ser
130           135           140
Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys Cys
145           150           155           160
Lys Glu Trp Val Cys Asp Glu Pro Lys Asp Arg Thr Ala Val Gly Pro
165           170           175
Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro Thr
180           185           190
Met Met Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala Cys
195           200           205
Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp Asn
210           215           220
Thr Phe Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg Pro
225           230           235           240
Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys Ile
245           250           255
Arg Thr Pro Lys Ile Ala Lys Pro Val Lys Phe Glu Leu Ser Gly Cys
260           265           270
Thr Ser Val Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr Asp
275           280           285
Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu Phe
290           295           300

```

Lys Cys Pro Asp Gly Glu Ile Met Lys Lys Asn Met Met Phe Ile Lys  
 305 310 315 320  
 Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe Glu  
 325 330 335  
 Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala  
 340 345

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2075 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (D) OTHER INFORMATION: "CTGF cDNA coding sequence"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

CCCCGCCGAC AGCCCCGAGA CGACAGCCCG GCGCGTCCCG GTCCCCACCT CCGACCACCG      60
CCAGCGCTCC AGGCCCCGCG CTCCCCGCTC GCCGCCACCG CGCCCTCCGC TCCGCCCGCA      120
GTGCCAACCA TGACCGCCGC CAGTATGGGC CCCGTCCGCG TCGCCTTCGT GGTCTCTCTC      180
GCCCTCTGCA GCCGGCCGGC CGTEGGCCAG AACTGCAGCG GGCCGTGCCG GTGCCCGGAC      240
GAGCCGGCGC CGCGCTGCCC GCGGGGCGTG AGCCTCGTGC TGGACGGCTG CGGCTGCTGC      300
CGCGTCTGCG CCAAGCAGCT GGGCGAGCTG TGCACCGAGC GCGACCCCTG CGACCCGCAC      360
AAGGGCCTCT TCTGTGACTT CGGCTCCCCG GCCAACCGCA AGATCGGCGT GTGCACCGCC      420
AAAGATGGTG CTCCCTGCAT CTTCGGTGGT ACGGTGTACC GCAGCGGAGA GTCCTTCCAG      480
AGCAGCTGCA AGTACCAAGT CACGTGCCTG GACGGGGCGG TGGGCTGCAT GCCCCTGTGC      540
AGCATGGACG TTCGTCTGCC CAGCCCTGAC TGCCCCTTCC CGAGGAGGGT CAAGCTGCCC      600
GGGAAATGCT GCGAGGAGTG GGTGTGTGAC GAGCCCCAAG ACCAAACCGT GGTGGGGCCT      660
GCCCTCGCGG CTTACCGACT GGAAGACACG TTTGGCCCAG ACCCAACTAT GATTAGAGCC      720
AACTGCCTGG TCCAGACCAC AGAGTGGAGC GCCTGTTCCT AGACCTGTGG GATGGGCATC      780
TCCACCCGGG TTACCAATGA CAACGCCTCC TGCAGGCTAG AGAAGCAGAG CCGCCTGTGC      840
ATGGTCAGGC CTTGCGAAGC TGACCTGGAA GAGAACATTA AGAAGGGCAA AAAGTGCATC      900
CGTACTCCCA AAATCTCCAA GCCTATCAAG TTTGAGCTTT CTGGCTGCAC CAGCATGAAG      960
ACATACCGAG CTAAATTCTG TGGAGTATGT ACCGACGGCC GATGCTGCAC CCCCCACAGA     1020
ACCACCACCC TGCCGGTGGA GTTCAAGTGC CCTGACGGCG AGGTCATGAA GAAGAACATG     1080
ATGTTTCATCA AGACCTGTGC CTGCCATTAC AACTGTCCCG GAGACAATGA CATCTTTGAA     1140

```

TCGCTGTACT ACAGGAAGAT GTACGGAGAC ATGGCATGAA GCCAGAGAGT GAGAGACATT	1200
AACTCATTAG ACTGGAACCTT GAACTGATTC ACATCTCATT TTTCCGTAAA AATGATTTCA	1260
GTAGCACAAG TTATTTAAAT CTGTTTTTCT AACTGGGGGA AAAGATTCCC ACCCAATTCA	1320
AAACATTGTG CCATGTCAAA CAAATAGTCT ATCTTCCCCA GACACTGGTT TGAAGAATGT	1380
TAAGACTTGA CAGTGGAACCT ACATTAGTAC ACAGCACCAG AATGTATATT AAGGTGTGGC	1440
TTTAGGAGCA GTGGGAGGGT ACCGGCCCCG TTAGTATCAT CAGATCGACT CTTATACGAG	1500
TAAATATGCCT GCTATTTGAA GTGTAATTGA GAAGGAAAAT TTTAGCGTGC TCACTGACCT	1560
GCCTGTAGCC CCACTGACAG CTAGGATGTG CATTCTCCAG CCATCAAGAG ACTGAGTCAA	1620
GTTGTTCCCTT AAGTCAGAAC AGCAGACTCA GCTCTGACAT TCTGATTCGA ATGACACTGT	1680
TCAGGAATCG GAATCCTGTC GATTAGACTG GACAGCTTGT GGCAAGTGAA TTTGCCTGTA	1740
ACAAGCCAGA TTTTTTAAAA TTTATATTGT AAATATTGTG TGTGTGTGTG TGTGTGTATA	1800
TATATATATA TATGTACAGT TATCTAAGTT AATTITAAAGT TGTGTGTGCC TTTTATTTT	1860
TGTTTTTAAT GCTTTGATAT TTCAATGTGA GCCTCAATTT CTGAACACCA TAGGTAGAAT	1920
GTAAAGCTTG TCTGATCGTT CAAAGCATGA AATGGATACT TATATGGAAA TTCTGCTCAG	1980
ATAGAATGAC AGTCCGTCAA AACAGATTGT TTGCAAAGGG GAGGCATCAG TGTCTTGGCA	2040
GGCTGATTTT TAGGTAGGAA ATGTGGTAGC TCACG	2075

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (D) OTHER INFORMATION: "CTGF amino acid sequence"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Thr	Ala	Ala	Ser	Met	Gly	Pro	Val	Arg	Val	Ala	Phe	Val	Val	Leu
1				5					10					15	
Leu	Ala	Leu	Cys	Ser	Arg	Pro	Ala	Val	Gly	Gln	Asn	Cys	Ser	Gly	Pro
		20						25					30		
Cys	Arg	Cys	Pro	Asp	Glu	Pro	Ala	Pro	Arg	Cys	Pro	Ala	Gly	Val	Ser
		35					40					45			
Leu	Val	Leu	Asp	Gly	Cys	Gly	Cys	Cys	Arg	Val	Cys	Ala	Lys	Gln	Leu
	50				55					60					
Gly	Glu	Leu	Cys	Thr	Glu	Arg	Asp	Pro	Cys	Asp	Pro	His	Lys	Gly	Leu
65					70			75						80	

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGGATCTGT GACGAGCCCA AGGAC

25

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGAATTCGA CCAGGCAGTT GGCTCG

26

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGGGATCCTG TGATGAAGAC AGCATT

26

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGAATTCAA CGATGCATTT CTGGCC

26

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asp Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp  
1 5 10 15  
Cys Ser Lys Thr Gln  
20

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val Gly Cys  
1 5 10 15  
Ile Pro Leu Cys Pro  
20

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser Cys Gly  
1 5 10 15  
Thr Gly Ile Ser Thr Arg Val Thr  
20

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ile	Ser	Thr	Arg	Val	Thr	Asn	Asp	Asn	Pro	Glu	Cys	Arg	Leu	Val	Lys
1				5					10					15	
Glu	Thr	Arg	Ile	Cys	Glu	Val	Arg	Pro	Cys						
			20					25							

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys	Tyr	Cys	Gly	Ser	Cys	Val	Asp	Gly	Arg	Cys	Cys	Thr	Pro	Leu	Gln
1				5					10					15	
Thr	Arg	Thr	Val	Lys											
			20												



**This Page is Inserted by IFW Indexing and Scanning  
Operations and is not part of the Official Record**

**BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ BLACK BORDERS
- ☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☐ FADED TEXT OR DRAWING
- ☒ BLURRED OR ILLEGIBLE TEXT OR DRAWING
- ☐ SKEWED/SLANTED IMAGES
- ☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☐ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☐ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: \_\_\_\_\_

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.**